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October 23, 2020

TO: ASSISTANT UNITED STATES ATTORNEY BRENDAN T. CONWAY
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PITTSBURGH, PA 15219

SUPPLEMENTAL REPORT
Cybergenetics: ACDA75
Lab: 18LAB06905
Agency: 18161793

Suspect: ELLIS, Lafon

Evidence Items:

Item 2A	Swabbing of pistol
Item 4	Reference of Lafon Ellis

METHODS:

- The DNA PowerPlex® Fusion 6C data profiles referenced in this report were previously developed and addressed in a Report of Laboratory Findings issued by the Allegheny County Office of the Medical Examiner.
- This report supplements a TrueAllele® Report issued by Cybergenetics on December 5, 2019.
- Each evidence item was analyzed using open source semi-continuous software LRmix (version 4.1), Lab Retriever (version 2.2.1), and likeLTD (version 5.5).
- Each evidence item was analyzed using open source continuous software likeLTD (version 6.3) and EuroForMix (version 3.1.0).
- The National Institute of Standards and Technology generated the population allele frequencies.
- The DNA match statistics herein were calculated at a theta value (co-ancestry coefficient) of 1%.
- All evidence genotypes were compared with all reference genotypes to compute likelihood ratio (LR) DNA match statistics.

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SETTINGS:

Item 2A, pistol

Software Input Settings

The following table describes the input settings for each software program. The data were analyzed assuming four contributors. When the software was limited to under four contributors, drop-in was considered.

Unknown contributor is abbreviated as 'unk' in the table below.

Input settings	LRmix	Lab Retriever	likeLTD, v 5.5	likeLTD, v 6.3	EuroForMix
Data threshold	50 rfu	50 rfu	50 rfu	20 rfu	50 rfu
Stutter modeled	No	No	No	Yes	Yes
Total loci used	22	21	16	16	21
Loci omitted	SE33	Penta D, Penta E	CSF1PO, D5S818, D7S820, D13S317, Penta D, Penta E, TPOX	D2S1338, D12S391, D18S51, D22S1045, Penta D, Penta E, SE33	Penta D, Penta E
Pr(Dropin)	0.05	0.01	TRUE	TRUE	0.05
Pr(Dropout)	0.1	0			
Degradation					Yes
H _p	suspect+3unk	suspect+3unk	suspect+2unk+dropin	suspect+2unk+dropin	suspect+3unk
H _d	4unk	4unk	3unk+dropin	3unk+dropin	4unk

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RESULTS:

Item 2A, pistol

DNA Match Tables

1. Likelihood ratio*

Item	Reference	LRmix	Lab Retriever	likeLTD, v 5.5	likeLTD, v 6.3	EuroForMix
2A	4	1.44 thousand	110 thousand	36.7 thousand	721 million	2.02 quadrillion

2. $\log_{10}(\text{LR})$, or the powers of ten in the LR number

Item	Reference	LRmix	Lab Retriever	likeLTD, v 5.5	likeLTD, v 6.3	EuroForMix
2A	4	3.16	5.04	4.57	8.86	15.31

*The LR shown is calculated using the African-American ethnic population.

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Appendix

The data were analyzed with open source software programs. Both *semi-continuous* (software that does not use peak heights) and *continuous* (software that uses peak heights) were used. The installers, manuals, and source code are available as described below.

Semi-continuous methods

LRmix

1. Haned H. Forensim: an open source initiative for the evaluation of statistical methods in forensic genetics. *Forensic Sci. Int. Genet.* 2010;5(4):265–268.
2. LRmix web document: <https://forensim.r-forge.r-project.org/misc/LRmix.pdf>
3. Forensim website: <http://forensim.r-forge.r-project.org/>

Lab Retriever

1. Inman K, Rudin N, Cheng K, Robinson C, Kirschner A, Inman-Semerau, L, Lohmueller KE. Lab Retriever: a software tool for calculating likelihood ratios incorporating a probability of drop-out for forensic DNA profiles. *BMC Bioinformatics.* 2015;16:298.
2. Lab Retriever website: <https://scieg.org/lab-retriever/>

likeLTD, version 5.5

1. Balding DJ. Evaluation of mixed-source, low-template DNA profiles in forensic science. *Proc Natl Acad Sci USA.* 2013;110(30):12241–46.
2. likeLTD website: <https://blogs.unimelb.edu.au/statisticalgenomics/publications-software/likeltd-software/>

Continuous methods

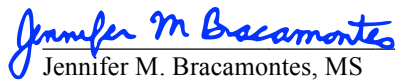
likeLTD, version 6.3


1. Steele C, Greenhalgh M, DJB. Evaluation of low-template DNA profiles using peak heights. *Statist Appl Genet Molec Biol.* 2016;15(5):431–45.
2. likeLTD website: <https://blogs.unimelb.edu.au/statisticalgenomics/publications-software/likeltd-software/>


EuroForMix

1. Cowell RG, Graversen T, Lauritzen SL, Mortera J. Analysis of forensic DNA mixtures with artefacts. *Appl. Statist.*, 2015;64(1):1–32.
2. Bleka Ø, Storvik G, Gill P. EuroForMix: An open source software based on a continuous model to evaluate STR DNA profiles from a mixture of contributors with artefacts. *Forensic Sci. Int. Genet.* 2016;21:35–44.
3. Bleka Ø, Benschop CC, Storvik G, Gill P. A comparative study of qualitative and quantitative models used to interpret complex STR DNA profiles. *Forensic Sci Int Genet.* 2016;25:85–96.
4. Bleka Ø, Eduardoff M, Santos C, Phillips C, Parson W, Gill P. Open source software EuroForMix can be used to analyse complex SNP mixtures. *Forensic Sci Int Genet.* 2017;31:105–110.
5. EuroForMix website: <http://www.euroformix.com/>

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